protein-like element, a transcriptional silencer, and a pair of purine-rich sequence motifs that were found in other T cell-specific genes, and three repeats of GGCCTG that may be a variation of a highly repetitious GCCCTG consensus sequence found in human Pfp.

L20 ANSWER 15 OF 29 MEDLINE on STN
ACCESSION NUMBER: 2000047738 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10580136
TITLE: O-GlcNAc and the control of gene expression.
AUTHOR: Comer F I; Hart G W
CORPORATE SOURCE: Department of Biological Chemistry, Johns Hopkins University School of Medicine, 725 N. Wolfe St., Baltimore, MD 21205, USA.
SOURCE: Biochimica et biophysica acta, ***(1999 Dec 6)*** Vol. 1473, No. 1, pp. 161-71. Ref: 56
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200001
ENTRY DATE: Entered STN: 24 Jan 2000
Last Updated on STN: 24 Jan 2000
Entered Medline: 11 Jan 2000

AB Many eukaryotic proteins contain O-linked N-acetylglucosamine (O-GlcNAc) on their serine and threonine side chain hydroxyls. In contrast to classical cell surface glycosylation, O-GlcNAc occurs on resident nuclear and cytoplasmic proteins. O-GlcNAc exists as a single monosaccharide residue, showing no evidence of further elongation. Like phosphorylation, O-GlcNAc is highly dynamic, transiently modifying proteins. These post-translational modifications give rise to functionally distinct subsets of a given protein. Furthermore, all known O-GlcNAc proteins are also phosphoproteins that reversibly form multimeric complexes that are sensitive to the state of phosphorylation. This observation implies that O-GlcNAc may work in concert with phosphorylation to mediate regulated protein interactions. The proteins that bear the O-GlcNAc modification are very diverse, including ***RNA polymerase*** II and many of its transcription factors, numerous chromatin-associated proteins, nuclear ***pore*** proteins, proto-oncogenes, tumor suppressors and proteins involved in translation. Here, we discuss the functional implications of O-GlcNAc-modifications of proteins involved in various aspects of gene expression, beginning with proteins involved in transcription and ending with proteins involved in regulating protein translation.

L20 ANSWER 16 OF 29 MEDLINE on STN
ACCESSION NUMBER: 97386819 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9242909
TITLE: Dynamic O-linked glycosylation of nuclear and cytoskeletal proteins.
AUTHOR: Hart G W
CORPORATE SOURCE: Department of Biochemistry and Molecular Genetics, University of Alabama at Birmingham, School of Medicine 35294-0005, USA.. gwhart@bmg.bhs.uab.edu
SOURCE: Annual review of biochemistry, ***(1997)*** Vol. 66, pp. 315-35. Ref: 190
Journal code: 2985150R. ISSN: 0066-4154.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199710

ENTRY DATE: Entered STN: 21 Oct 1997
Last Updated on STN: 21 Oct 1997
Entered Medline: 7 Oct 1997

AB Modification of Ser and Thr residues by attachment of O-linked N-acetylglucos-amine [Ser(Thr)-O-GlcNAcylation] to eukaryotic nuclear and cytosolic proteins is as dynamic and possibly as abundant as Ser(Thr) phosphorylation. Known O-GlcNAcylated proteins include cytoskeletal proteins and their regulatory proteins; viral proteins; nuclear-***pore***, heat-shock, tumor-suppressor, and nuclearoncogene proteins; ***RNA polymerase*** II catalytic subunit; and a multitude of transcription factors. Although functionally diverse, all of these proteins are also phosphoproteins. Most O-GlcNAcylated proteins form highly regulated multimeric associations that are dependent upon their posttranslational modifications. Evidence is mounting that O-GlcNAcylation is an important regulatory modification that may have a reciprocal relationship with O-phosphorylation and may modulate many biological processes in eukaryotes.

L20 ANSWER 17 OF 29 MEDLINE on STN
ACCESSION NUMBER: 95133140 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7831765
TITLE: The metabolism of small cellular RNA species during productive subgroup C adenovirus infection.
AUTHOR: Smiley J K; Young M A; Bansbach C C; Flint S J
CORPORATE SOURCE: Department of Molecular Biology, Princeton University, New Jersey 08544-1014.
SOURCE: Virology, ***(1995 Jan 10)*** Vol. 206, No. 1, pp. 100-7.
Journal code: 0110674. ISSN: 0042-6822.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE) (RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199502
ENTRY DATE: Entered STN: 7 Mar 1995
Last Updated on STN: 3 Feb 1997
Entered Medline: 17 Feb 1995

AB During the late phase of subgroup C adenovirus infection, export of cellular mRNA from the nucleus to the cytoplasm is inhibited. In one approach to investigate the mechanism whereby viral late mRNAs are selected for export, we have examined the metabolism of small cellular RNA species transcribed by all three RNA polymerases during the late phase of Ad5 infection. No changes in the quantities of [3H]uridine-labeled 5S rRNA or tRNAs entering the cytoplasm were observed in infected cells. Adenovirus type 5 infection reduced the nuclear and cytoplasmic populations of the newly synthesized, snRNP-associated snRNAs U1, U2, U4, U5, and U6. Transcription of a representative snRNA, U1 RNA, was not inhibited, indicating that the post-transcriptional metabolism of snRNAs was perturbed during the late phase of infection. The increased cytoplasmic concentration of newly synthesized U1 RNA in Ad5- compared to mock-infected cells, and the greater reduction of the snRNP-associated compared to the total U1 RNA population, indicated that snRNP assembly in the cytoplasm was impaired. As adenovirus infection does not perturb export from the nucleus of small cellular mRNAs transcribed by ***RNA polymerases*** II and III, viral mRNA must be distinguished for selective export at a nuclear step upstream of translocation to the cytoplasm via nuclear ***pore*** complexes.

L20 ANSWER 18 OF 29 MEDLINE on STN
ACCESSION NUMBER: 94375512 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8089168
TITLE: An RNase-sensitive particle containing Drosophila melanogaster DNA topoisomerase II.

AUTHOR: Meller V H; McConnell M; Fisher P A
CORPORATE SOURCE: Department of Pharmacological Sciences, University Medical Center, State University of New York at Stony Brook 11794-8651.
CONTRACT NUMBER: F32 CA09052 (NCI)
SOURCE: The Journal of cell biology, ***(1994 Sep)*** Vol. 126, No. 6, pp. 1331-40.
Journal code: 0375356. ISSN: 0021-9525.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199410
ENTRY DATE: Entered STN: 31 Oct 1994
Last Updated on STN: 31 Oct 1994
Entered Medline: 14 Oct 1994

AB Most DNA topoisomerase II (topo II) in cell-free extracts of 0-2-h old Drosophila embryos appears to be nonnuclear and remains in the supernatant after low-speed centrifugation (10,000 g). Virtually all of this apparently soluble topo II is particulate with a sedimentation coefficient of 67 S. Similar topo II-containing particles were detected in Drosophila Kc tissue culture cells, 16-19-h old embryos and extracts of progesterone-matured oocytes from Xenopus. Drosophila topo II-containing particles were insensitive to EDTA, Triton X-100 and DNase I, but could be disrupted by incubation with 0.3 M NaCl or RNase A. After either disruptive treatment, topo II sedimented at 9 S. topo II-containing particles were also sensitive to micrococcal nuclease. Results of chemical cross-linking corroborated those obtained by centrifugation. Immunoblot analyses demonstrated that topo II-containing particles lacked significant amounts of lamin, nuclear ***pore*** complex protein gp210, proliferating cell nuclear antigen, ***RNA polymerase*** II subunits, histones, coilin, and nucleolin. Northern blot analyses demonstrated that topo II-containing particles lacked U RNA. Thus, current data support the notion that nonnuclear Drosophila topo II-containing particles are composed largely of topo II and an unknown RNA molecule(s).

L20 ANSWER 19 OF 29 MEDLINE on STN
ACCESSION NUMBER: 94316601 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8041713
TITLE: Yeast Srp1p has homology to armadillo/plakoglobin/beta-catenin and participates in apparently multiple nuclear functions including the maintenance of the nucleolar structure.
AUTHOR: Yano R; Oakes M L; Tabb M M; Nomura M
CORPORATE SOURCE: Department of Biological Chemistry, University of California, Irvine 91717-1700.
CONTRACT NUMBER: GM0713419 (NIGMS)
R37GM35949 (NIGMS)
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, ***(1994 Jul 19)*** Vol. 91, No. 15, pp. 6880-4.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199408
ENTRY DATE: Entered STN: 5 Sep 1994
Last Updated on STN: 5 Sep 1994
Entered Medline: 22 Aug 1994

AB SRP1, a suppressor of certain temperature-sensitive mutations in

RNA polymerase I in Saccharomyces cerevisiae, encodes a protein that is associated with nuclear ***pores***. By using a system of conditional SRP1 expression and by isolating temperature-sensitive srp1 mutants, we have demonstrated that Srp1p is essential for maintenance of the crescent-shaped nucleolar structure, RNA transcription, and the proper functions of microtubules as inferred from analysis of nuclear division/segregation and immunofluorescence microscopy of microtubules. Different mutant alleles showed significantly different phenotypes in relation to these apparently multiple functional roles of the protein. We have also found that eight imperfect 42-amino-acid tandem repeats present in Srp1p are similar to the 42-amino-acid repeats in armadillo/plakoglobin/beta-catenin proteins present in adhesive junction complexes of higher eukaryotes. We discuss this similarity in connection with the observed pleiotropic effects of srp1 mutations.

L20 ANSWER 20 OF 29 MEDLINE on STN
ACCESSION NUMBER: 91178442 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1840607
TITLE: Structure of the mouse pore-forming protein (perforin) gene: analysis of transcription initiation site, 5' flanking sequence, and alternative splicing of 5' untranslated regions.
AUTHOR: Youn B S; Liu C C; Kim K K; Young J D; Kwon M H; Kwon B S
CORPORATE SOURCE: Department of Microbiology and Immunology, Indiana University School of Medicine, Indianapolis 46202.
CONTRACT NUMBER: AI-28175 (NIAID)
AR-40248 (NIAMS)
DK-20542 (NIDDK)
+
SOURCE: The Journal of experimental medicine, ***(1991 Apr 1)*** Vol. 173, No. 4, pp. 813-22.
Journal code: 2985109R. ISSN: 0022-1007.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X54781; GENBANK-X54782; GENBANK-X54783; GENBANK-X54784; GENBANK-X56613; GENBANK-X58602; GENBANK-X58603; GENBANK-X58604; GENBANK-X58605; GENBANK-X58606
ENTRY MONTH: 199104
ENTRY DATE: Entered STN: 19 May 1991
Last Updated on STN: 19 May 1991
Entered Medline: 26 Apr 1991

AB We studied the 5' untranslated regions (UTRs) of the mouse lymphocyte ***pore***-forming protein (PFP, perforin, and cytolysin). 5' UTRs were determined by primer extension analysis, sequencing PFP cDNA clone PFP-7, ribonuclease protection assays, and amplification of poly(A)+ ***RNA*** of cytolytic T lymphocyte using ***polymerase*** chain reaction (PCR). Two alternatively spliced 5' UTRs, designated type I and type II, of 222 and 115 bp, respectively, were found associated with PFP. Type II is identical to type I, except for being 107 bp shorter in the second exon. This deletion was generated by the use of alternative acceptor splice sites. The mouse PFP gene (Pfp) encodes three exons, is separated by two small introns, and spans a chromosomal region of approximately 7 kb. The first exon contains 79 bp of 5' UTR, the second exon contains 143 or 36 bp of 5' UTR (type I or type II UTR, respectively) plus the NH2-terminal region of the mouse PFP, and the third exon contains the rest of the COOH-terminal mouse PFP. The organization of the mouse Pfp is similar to that of the human gene. Moreover, the 5' flanking sequence of the mouse Pfp is highly homologous to that of the human Pfp. In contrast to the human sequence, the more immediate 5' flanking sequence of mouse Pfp

contains two tandem "TATA" box-related elements and a GC box, but lacks a typical CAAT box-related sequence. Several other enhancer elements were found further upstream, including cAMP-, phorbol ester-, interferon-gamma-, and UV-responsive elements, and PU box-like and NFkB binding site-like elements. In addition, we found a nuclear inhibitory protein-like element, a transcriptional silencer, and a pair of purine-rich sequence motifs that were found in other T cell-specific genes, and three repeats of GGCCTG that may be a variation of a highly repetitious GCCCTG consensus sequence found in human Pfp.

L20 ANSWER 21 OF 29 HCAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2001:519443 HCAPLUS
DOCUMENT NUMBER: 135:103844
TITLE: O-glycosylation of nuclear proteins
AUTHOR(S): Krzeslak, Anna; Lipinska, Anna
CORPORATE SOURCE: Katedra Cytobiochem., Uniw. Lodzki, Lodz, 90-237, Pol.
SOURCE: Postepy Biologii Komorki (*2000*), 27(3), 441-460
CODEN: PBKODV; ISSN: 0324-833X
PUBLISHER: Fundacja Biologii Komorki i Biologii Molekularnej
DOCUMENT TYPE: Journal; General Review
LANGUAGE: Polish
AB A review with 80 refs. Glycosylation, consisting in incorporation of single N-acetylglucosamine residues attached by O-linkage to serine or threonine residues, is a common modification of nuclear proteins. Numerous chromatin and nuclear ***pore*** complex proteins as well as ***RNA polymerase*** II and some transcription factors are glycosylated in this unusual way. O-glycosylation of nuclear proteins has been postulated to play a role in nucleus-cytoplasmic transport, transcriptional regulation and regulation of protein phosphorylation level. In this paper data concerning enzymes engaged in O-glycosylation and deglycosylation of proteins, attachment sites of N-acetylglucosamine residues and known nuclear glycoproteins have been described.

L20 ANSWER 22 OF 29 HCAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2000:412428 HCAPLUS
DOCUMENT NUMBER: 133:173725
TITLE: Engines of gene expression
AUTHOR(S): Geiduschek, E. Peter; Bartlett, Michael S.
CORPORATE SOURCE: Department of Biology and Center for Molecular Genetics, University of California, San Diego, La Jolla, CA, 92093-0634, USA
SOURCE: Nature Structural Biology (*2000*), 7(6), 437-439
CODEN: NSBIEW; ISSN: 1072-8368
PUBLISHER: Nature America Inc.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review and discussion with 20 refs. A backbone model of ten subunits of yeast RNA polymerase II has been derived from the ongoing anal. of its crystal structure. Notable features include "jaws" for holding DNA, a putatively RNA-regulated "sliding clamp", two "***pores***" located in the vicinity of the catalytic center, and a high degree of similarity with the structure of a bacterial ***RNA polymerase***.
REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 23 OF 29 HCAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2000:101138 HCAPLUS
DOCUMENT NUMBER: 133:41131
TITLE: Dynamic cytoskeletal glycosylation and neurodegenerative disease
AUTHOR(S): Arnold, C. Shane; Hart, Gerald W.
CORPORATE SOURCE: Dept. of Biological Chemistry The Johns Hopkins

University School of Medicine, Baltimore, MD, 21205, USA
SOURCE: Trends in Glycoscience and Glycotechnology (*1999*), 11(62), 355-370
CODEN: TGGLEE; ISSN: 0915-7352
PUBLISHER: FCCA
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review, with 116 refs. O-GlcNAcylation of nucleoplasmic and cytoplasmic proteins is a ubiquitous and highly dynamic modification. It entails the attachment of a single O-linked N-acetylglucosamine (O-GlcNAc) moiety O-glycosidically linked to side-chain hydroxyls of serine and threonine residues. The rapidly expanding list of O-GlcNAcylated proteins includes ***RNA polymerase*** II; nuclear ***pore***, heat-shock, and tumor suppressor proteins; nuclear oncogenes; and numerous cytoskeletal and membrane-associated proteins. Many sites of O-GlcNAc addition are similar to consensus sites of protein phosphorylation and, in some cases, identical. Accordingly, O-GlcNAcylation and O-phosphorylation appear to be reciprocally related on some proteins. All O-GlcNAcylated proteins are phosphoproteins which assemble into tightly regulated reversible multi-protein complexes. Several O-GlcNAcylated proteins are key components involved in cytoskeletal assembly and organization, and defects in their regulated multimerization are implicated in several neurodegenerative disorders. Thus, abnormal cytoskeletal O-GlcNAcylation may promote defects in regulated protein multimerization and potentiate disease.
REFERENCE COUNT: 116 THERE ARE 116 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 24 OF 29 HCAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1999:746565 HCAPLUS
DOCUMENT NUMBER: 132:88785
TITLE: O-GlcNAc and the control of gene expression
AUTHOR(S): Comer, F. I.; Hart, G. W.
CORPORATE SOURCE: Department of Biological Chemistry, Johns Hopkins University School of Medicine, Baltimore, MD, USA
SOURCE: Biochimica et Biophysica Acta, General Subjects (*1999*), 1473(1), 161-171
CODEN: BBGSB3; ISSN: 0304-4165
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review with 56 refs. Many eukaryotic proteins contain O-linked N-acetylglucosamine (O-GlcNAc) on their Ser and Thr side-chain OH groups. In contrast to classical cell surface glycosylation, O-GlcNAc occurs on resident nuclear and cytoplasmic proteins. O-GlcNAc exists as a single monosaccharide residue, showing no evidence of further elongation. Like phosphorylation, O-GlcNAc is highly dynamic, transiently modifying proteins. These post-translational modifications give rise to functionally distinct subsets of a given protein. Furthermore, all known O-GlcNAc proteins are also phosphoproteins that reversibly form multimeric. complexes that are sensitive to the state of phosphorylation. This observation implies that O-GlcNAc may work in concert with phosphorylation to mediate regulated protein interactions. The proteins that bear the O-GlcNAc modification are very diverse, including ***RNA polymerase*** II and many of its transcription factors, numerous chromatin-associated proteins, nuclear ***pore*** proteins, proto-oncogenes, tumor suppressors, and proteins involved in translation. Here, the authors discuss the functional implications of O-GlcNAc-modifications of proteins involved in various aspects of gene expression, beginning with proteins involved in transcription and ending with proteins involved in regulating protein translation.
REFERENCE COUNT: 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 25 OF 29 HCAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1997:417199 HCAPLUS
DOCUMENT NUMBER: 127:157981
TITLE: Dynamic O-linked glycosylation of nuclear and cytoskeletal proteins
AUTHOR(S): Hart, Gerald W.
CORPORATE SOURCE: Dep. Biochem. and Molecular Genetics, Univ. Alabama, Sch. Med. and Dentistry, Birmingham, AL, 35294-0005, USA
SOURCE: Annual Review of Biochemistry (*1997*), 66, 315-335
CODEN: ARBOAW; ISSN: 0066-4154
PUBLISHER: Annual Reviews
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review, with 190 refs. Modification of Ser and Thr residues by attachment of O-linked N-acetylglucosamine [Ser(Thr)-O-GlcNAcylation] to eukaryotic nuclear and cytosolic proteins is as dynamic and possibly as abundant as Ser(Thr) phosphorylation. Known O-GlcNAcylated proteins include cytoskeletal proteins and their regulatory proteins; viral proteins; nuclear-***pore***, heat-shock, tumor-suppressor, and nuclear-oncogene proteins; ***RNA polymerase*** II catalytic subunit; and a multitude of transcription factors. Although functionally diverse, all of these proteins are also phosphoproteins. Most O-GlcNAcylated proteins form highly regulated multimeric assocns. that are dependent upon their posttranslational modifications. Evidence is mounting that O-GlcNAcylation is an important regulatory modification that may have a reciprocal relation with O-phosphorylation and may modulate many biol. processes in eukaryotes.

L20 ANSWER 26 OF 29 HCAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1996:721885 HCAPLUS
DOCUMENT NUMBER: 126:4207
TITLE: Characterization of individual polymer molecules based on monomer-interface interactions
INVENTOR(S): Church, George; Deamer, David W.; Branton, Daniel; Baldarelli, Richard; Kasianowicz, John
PATENT ASSIGNEE(S): President and Fellows of Harvard College, USA
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9629593	A1	19960926	WO 1996-US2937	19960301 <--
W: CA, JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 815438	A1	19980107	EP 1996-909569	19960301 <--
R: DE, FR, GB, IT				
US 2003044816	A1	20030306	US 2002-79178	20020220
US 6673615	B2	20040106		
US 2005053961	A1	20050310	US 2003-739585	20031218
US 7189503	B2	20070313		

PRIORITY APPLN. INFO.:

US 1995-405735	A	19950317
WO 1996-US2937	W	19960301
US 1998-98142	A2	19980616
US 1999-457959	A1	19991209
US 2002-79178	A1	20020220

AB A method is disclosed for characterizing a linear polymer mol., especially DNA

and RNA, by measuring phys. changes across an interface between two pools of media as the linear polymer traverses the interface and monomers of the polymer interact with the interface, where the phys. changes are suitable to identify characteristics of the polymer, e.g., polymer size or sequence. In one embodiment, the method involves measurements of ionic current modulation as, e.g., the nucleotides of a nucleic acid mol. pass through or across a channel in an artificial membrane. During polymer passage through or across the channel, ionic currents are reduced in a manner that reflects the properties of the polymer (e.g., length, concentration of polymers in solution, etc.) and the identities of the monomers. In a second embodiment, an immiscible interface is created between 2 immiscible liqs., and, as above, polymer passage through the interface results in monomer interactions with the interface that are sufficient to identify characteristics of the polymer and/or the identity of the monomers.

L20 ANSWER 27 OF 29 HCAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1995:450760 HCAPLUS
DOCUMENT NUMBER: 122:211031
TITLE: The metabolism of small cellular RNA species during productive subgroup C adenovirus infection
AUTHOR(S): Smiley, Jean K.; Young, Marjorie A.; Bansbach, Catherine C.; Flint, S. J.
CORPORATE SOURCE: Department Molecular Biology, Princeton University, Princeton, NJ, 08544-1014, USA
SOURCE: Virology (*1995*), 206(1), 100-7
CODEN: VIRLAX; ISSN: 0042-6822
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English
AB During the late phase of subgroup C adenovirus infection, export of cellular mRNA from the nucleus to the cytoplasm is inhibited. In one approach to investigate the mechanism whereby viral late mRNAs are selected for export, we have examined the metabolism of small cellular RNA species transcribed by all three RNA polymerases during the late phase of Ad5 infection. No changes in the quantities of [3H]uridine-labeled 5S rRNA or tRNAs entering the cytoplasm were observed in infected cells. Adenovirus type 5 infection reduced the nuclear and cytoplasmic populations of the newly synthesized, snRNP-associated snRNAs U1, U2, U4, U5, and U6. Transcription of a representative snRNA, U1 RNA, was not inhibited, indicating that the post-transcriptional metabolism of snRNAs was perturbed during the late phase of infection. The increased cytoplasmic concentration of newly synthesized U1 RNA in Ad5- compared to mock-infected cells, and the greater reduction of the snRNP-associated compared to the total U1
RNA population, indicated that snRNP assembly in the cytoplasm was impaired. As adenovirus infection does not perturb export from the nucleus of small cellular mRNAs transcribed by ***RNA polymerases*** II and III, viral mRNA must be distinguished for selective export at a nuclear step upstream of translocation to the cytoplasm via nuclear ***pore*** complexes.

L20 ANSWER 28 OF 29 HCAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1994:528438 HCAPLUS
DOCUMENT NUMBER: 121:128438
TITLE: An RNase-sensitive particle containing Drosophila melanogaster DNA topoisomerase II
AUTHOR(S): Meller, Victoria H.; McConnell, Maeve; Fisher, Paul A.
CORPORATE SOURCE: Univ. Med. Cent., State Univ. New York, Stony Brook, NY, 11794-8651, USA
SOURCE: Journal of Cell Biology (*1994*), 126(6), 1331-40
CODEN: JCLBA3; ISSN: 0021-9525
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Most DNA topoisomerase II (topo II) in cell-free exts. of 0-2 h old Drosophila embryos appears to be nonnuclear and remains in the supernatant after low-speed centrifugation (10,000 g). Virtually all of this apparently soluble topo II is particulate with a sedimentation coefficient of 67
S. Similar topo II-containing particles were detected in Drosophila Kc tissue culture cells, 16-19 h old embryos and exts. of progesterone-matured oocytes from Xenopus. Drosophila topo II-containing particles were insensitive to EDTA, Triton X-100 and DNase I, but could be disrupted by incubation with 0.3 M NaCl or RNase A. After either disruptive treatment, topo II sedimented at 9 S. topo II-containing particles were also sensitive to micrococcal nuclease. Results of chemical crosslinking corroborated those obtained by centrifugation. Immunoblot analyses demonstrated that topo II-containing particles lacked significant amts. of lamin, nuclear ***pore*** complex protein gp210, proliferating cell nuclear antigen, ***RNA polymerase*** II subunits, histones, coilin, and nucleolin. Northern blot analyses demonstrated that topo II-containing particles lacked U RNA. Thus, current data support the notion that nonnuclear Drosophila topo II-containing particles are composed largely of topo II and an unknown RNA mol.(s).

L20 ANSWER 29 OF 29 HCAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1994:526890 HCAPLUS
DOCUMENT NUMBER: 121:126890
TITLE: Yeast Srp1p has homology to armadillo/plakoglobin/β-catenin and participates in apparently multiple nuclear functions including the maintenance of the nucleolar structure
AUTHOR(S): Yano, Ryoji; Oakes, Melanie L.; Tabb, Michelle M.; Nomura, Masayasu
CORPORATE SOURCE: Dep. Biol. Chem., Univ. California, Irvine, CA, 91717-1700, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (***1994***), 91(15), 6880-4
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English
AB SRP1, a suppressor of certain temperature-sensitive mutations in ***RNA polymerase*** I in Saccharomyces cerevisiae, encodes a protein that is associated with nuclear ***pores***. By using a system of conditional SRP1 expression and by isolating temperature-sensitive srp1 mutants, the authors have demonstrated that Srp1p is essential for maintenance of the crescent-shaped nucleolar structure, RNA transcription, and the proper functions of microtubules as inferred from anal. of nuclear division/segregation and immunofluorescence microscopy of microtubules. Different mutant alleles showed significantly different phenotypes in relation to these apparently that eight imperfect 42-amino-acid tandem repeats present in Srp1p are similar to the 42-amino-acid repeats in armadillo/plakoglobin/β-catenin proteins present in adhesive junction complexes of higher eukaryotes. The authors discuss this similarity in connection with the observed pleiotropic effects of srp1 mutations.

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INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 11:00:19 ON 03 OCT 2007

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0* FILE FROSTI
0* FILE FSTA
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0* FILE KOSMET
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5 FILE WPINDEX

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SEA ((EMBRYONIC STEM CELL) OR HES) AND CYP3A4 AND ALBUMIN

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2 FILE ESBIOBASE
6 FILE IFIPAT
1 FILE LIFESCI
2 FILE MEDLINE
1 FILE PASCAL
2 FILE SCISEARCH
49 FILE USPATFULL
4 FILE USPAT2
5 FILE WPIDS
5 FILE WPINDEX

L2 QUE ((EMBRYONIC STEM CELL) OR HES) AND CYP3A4 AND ALBUMIN

FILE 'BIOSIS, HCAPLUS, EMBASE, LIFESCI, MEDLINE, SCISEARCH' ENTERED AT 11:05:39 ON 03 OCT 2007

L3 13 S L2
L4 5 DUP REM L3 (8 DUPLICATES REMOVED)
L5 1 S ((EMBRYONIC STEM CELL) OR HES) AND CYP3A4 AND ALBUMIN AND PRO
L6 50 S ((EMBRYONIC STEM CELL) OR HES) AND (DRUG (W) (TESTING OR SCRE
L7 64193 S L6 AND METABOLIC OR TOXICOLOGIC
L8 8 S L6 AND (METABOLIC OR TOXICOLOGIC)
L9 9 S L6 AND PROMOTER
L10 4 S L6 AND REPORTER

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:01:38 ON 03 OCT 2007

SEA RNA(5A) POLYMERASE (P) SECONDARY CHANNEL

0* FILE ADISNEWS
3 FILE AGRICOLA
0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
14 FILE BIOSIS
1* FILE BIOTECHABS
1* FILE BIOTECHDS
2* FILE BIOTECHNO
17 FILE CAPLUS
1* FILE CEABA-VTB
0* FILE CIN
1 FILE CONFSCI
11 FILE DGENE
1 FILE DISSABS
13 FILE EMBASE
11* FILE ESBIOBASE
0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI
0* FILE FSTA
12 FILE GENBANK
0* FILE KOSMET
14 FILE LIFESCI
13 FILE MEDLINE
0* FILE NTIS
0* FILE NUTRACEUT
1* FILE PASCAL
0* FILE PHARMAML
17 FILE SCISEARCH
3 FILE TOXCENTER
1 FILE USPATFULL
0* FILE WATER
1 FILE WPIDS
1 FILE WPIFV
1 FILE WPINDEX

L11 QUE RNA(5A) POLYMERASE (P) SECONDARY CHANNEL

SEA RNA(5A) POLYMERASE (P) NTP(2A) UPTAKE(W) CHANNEL

0* FILE ADISNEWS
0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
1 FILE BIOSIS
0* FILE BIOTECHABS
0* FILE BIOTECHDS

```
  0*  FILE BIOTECHNO
  1   FILE CAPLUS
  0*  FILE CEABA-VTB
  0*  FILE CIN
  1   FILE EMBASE
  0*  FILE ESBIOBASE
  0*  FILE FOMAD
  0*  FILE FOREGE
  0*  FILE FROSTI
  0*  FILE FSTA
115   FILE GENBANK
  0*  FILE KOSMET
  1   FILE LIFESCI
  1   FILE MEDLINE
  0*  FILE NTIS
  0*  FILE NUTRACEUT
  0*  FILE PASCAL
  0*  FILE PHARMAML
  1   FILE SCISEARCH
  0*  FILE WATER
L12   QUE RNA(5A) POLYMERASE (P) NTP(2A) UPTAKE(W) CHANNEL
      ---------
      SEA RNA(5A) POLYMERASE (P) PORE
      ---------
  0*  FILE ADISNEWS
  6   FILE AGRICOLA
  0*  FILE ANTE
  0*  FILE AQUALINE
  2   FILE AQUASCI
  4*  FILE BIOENG
 63   FILE BIOSIS
 22*  FILE BIOTECHABS
 22*  FILE BIOTECHDS
 36*  FILE BIOTECHNO
  2   FILE CABA
 67   FILE CAPLUS
  0*  FILE CEABA-VTB
  0*  FILE CIN
  8   FILE DGENE
  9   FILE DISSABS
  3   FILE DRUGU
 50   FILE EMBASE
 42*  FILE ESBIOBASE
  0*  FILE FOMAD
  0*  FILE FOREGE
  0*  FILE FROSTI
  0*  FILE FSTA
193   FILE GENBANK
 30   FILE IFIPAT
  0*  FILE KOSMET
 34   FILE LIFESCI
 51   FILE MEDLINE
  2*  FILE NTIS
  0*  FILE NUTRACEUT
  5*  FILE PASCAL
  0*  FILE PHARMAML
 95   FILE SCISEARCH
 14   FILE TOXCENTER
189   FILE USPATFULL
 24   FILE USPAT2
  0*  FILE WATER
 16   FILE WPIDS
 16   FILE WPINDEX
L13     QUE RNA(5A) POLYMERASE (P) PORE
```

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                ---------
                 SEA L12 AND L13
                ---------
                0*   FILE ADISNEWS
                0*   FILE ANTE
                0*   FILE AQUALINE
                0*   FILE BIOENG
                1    FILE BIOSIS
                0*   FILE BIOTECHABS
                0*   FILE BIOTECHDS
                0*   FILE BIOTECHNO
                1    FILE CAPLUS
                0*   FILE CEABA-VTB
                0*   FILE CIN
                1    FILE EMBASE
                0*   FILE ESBIOBASE
                0*   FILE FOMAD
                0*   FILE FOREGE
                0*   FILE FROSTI
                0*   FILE FSTA
               12    FILE GENBANK
                0*   FILE KOSMET
                1    FILE LIFESCI
                1    FILE MEDLINE
                0*   FILE NTIS
                0*   FILE NUTRACEUT
                0*   FILE PASCAL
                0*   FILE PHARMAML
                1    FILE SCISEARCH
                0*   FILE WATER
L14              QUE L12 AND L13
                ---------

     FILE 'BIOSIS, EMBASE, MEDLINE, HCAPLUS' ENTERED AT 13:11:08 ON 03 OCT 2007
L15           30 S RNA(5A)POLYMERASE (S) SECONDARY CHANNEL
L16            0 S L1 AND PY<2001
L17            0 S L15 AND PY<2001
L18            1 S RNA(5A) POLYMERASE (S) NTP(2A)UPTAKE(W)CHANNEL
L19           77 S RNA(5A)POLYMERASE (S) PORE
L20           29 S L19 AND PY<2001
L21       16178 S (MICROCIN OR (MCBA PROTEIN) OR (MCC25 PROTEIN) OR (MCCJ25) OR
L22            0 S L21 AND L20
L23            0 S L19 AND L21
L24            5 S RNA(5A) POLYMERASE (S) (SECONDARY CHANNEL) AND MICROCIN
L25            5 S RNA(5A) POLYMERASE (S) (SECONDARY CHANNEL) AND L21
L26            0 S L25 AND (SCREEN? OR IDENTIFY?)
L27            5 S L25 AND (INHIBIT? OR BIND? OR SUPPRESS?)
```